In This Issue

In Review: Human APOBEC3-HIV Restrictome

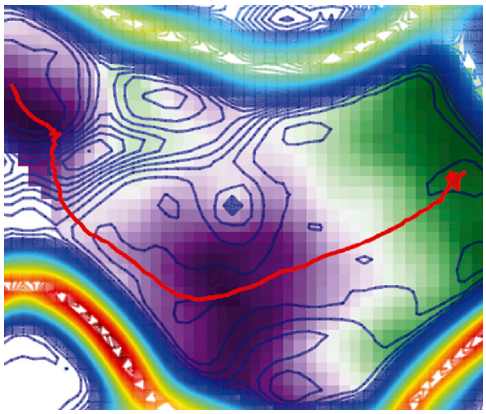
PAGE 668

The human APOBEC3 family proteins serve as front-line host-innate restriction factors that can inhibit the replication of a broad range of human and animal retroviruses. Aydin et al. summarize recent APOBEC3 structural and functional studies to provide new insights into its mechanisms of antiviral activity.

Rotational Assembly of Type IV Pilus-like Fibers

PAGE 685

Type IV pili and pseudopili are helical fibers that promote bacterial motility, adhesion, and macromolecular transport. Nivaskumar et al. identify the crucial role of twist forces in conformational transitions leading to pseudopilus assembly and suggest a rotational assembly mechanism for the type IV pili.



New Dimension of Actin-Vinculin Relationship

PAGE 697

The interaction of vinculin with F-actin plays a critical role in regulation of cell morphology and motility. Thompson et al. identify a surface on the vinculin tail domain critical for this interaction and show that actin-binding-deficient vinculin variants exhibit defects in cell spreading.

Special Delivery of a Toxic Ribosomal RNase

PAGE 707

Contact-dependent growth inhibition (CDI) systems deliver toxins to mediate interbacterial competition. Beck et al. show that the CDI toxin from *Enterobacter* cloacae cleaves 16S rRNA to inhibit cell growth. Because it's not related to known ribosomal RNases, CDI toxin reveals unexpected diversity in these enzymes.

Structure and Function of RNase AS

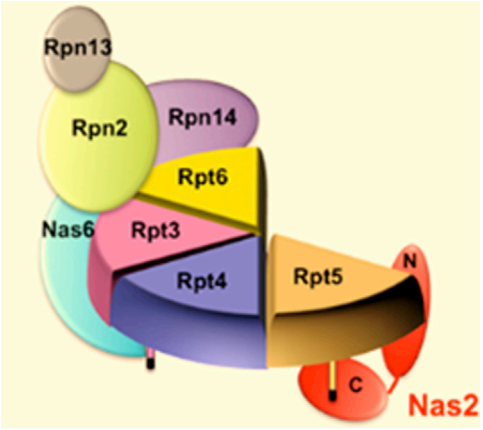
PAGE 719

Romano et al. characterize a key enzyme of *M. tuberculosis*, RNase AS, which strongly impacts virulence in vivo. This enzyme acts as a 3'-5'-exoribonuclease that specifically hydrolyzes adenylate-containing RNA sequences and structure points to a novel mechanism of substrate recruitment as a basis for specificity.

Proteasome under Control

PAGE 731

Assembly of the eukaryotic 26S proteasome is not due to spontaneous self-organization but results from a highly ordered process assisted by client-specific assembly chaperones. Satoh et al. provide a structural basis for working mechanisms of Nas2, providing the key missing link in the proteasome assembly pathway.



Phosphoinositide and Human Inositol Polyphosphate 5-Phosphatases

PAGE 744

Trésaugues et al. describe structures of apo-OCRL, apo-SHIP2, and INPP5B in complex with product analogs and unravel determinants of substrate selectivity and membrane-interacting regions in the phophosinositide 5-phosphatases family. The model suggests a different orientation of the substrate in the active site.

Being Strict about Monomethylation

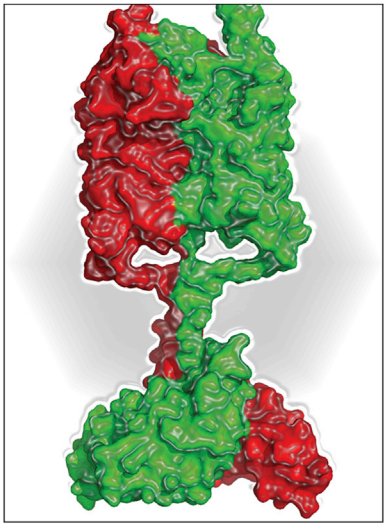
PAGE 756

Wang et al. report a crystal structure of *Trypanosoma brucei* TbPRMT7-AdoHcy complex with a histone H4 peptide substrate. The ternary complex combined with biochemical results and structural modeling reveals the structural basis for the strict arginine monomethylation activity of TbPRMT7.

Extracellular Loop: The Gatekeeper of PutP

PAGE 769

Using EPR spectroscopy, Raba et al. examine extracellular loop 4 of the Na^+/proline symporter PutP. The results suggest that the loop forms part of the extracellular gate and coordinates key steps of the transport by transmitting ligand-induced conformational changes to other domains of the transporter.



Mass Spectrometry Tackles Structure of Full-Length OmpA

PAGE 781

Marcoux et al. use an integrative approach including site-directed mutagenesis, cross-linking, native mass spectrometry, and ion mobility to localize the dimeric interface of OmpA. Combination of diverse insights allows the authors to propose a low-resolution model for the full-length OmpA dimer.

Short Article: Highly Coordinated

PAGE 791

Gram-negative bacteria rely on the ExbB–ExbD–TonB membrane protein complex for the import of essential nutrients leading to disease. Sverzhinsky et al. examine an ExbB (the scaffold protein) complex with ExbD (responsible for charging TonB) to reveal inherent structural flexibility and subunit rearrangements.

